



SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Reiter, Robert
Witte, Owen
- (ii) TITLE OF THE INVENTION: PSCA: Prostate Stem Cell Antigen
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Mandel & Adriano
(B) STREET: 35 N. Arroyo Parkway, Suite 60
(C) CITY: Pasadena
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 91103
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/038,261
(B) FILING DATE: 10-MAR-1998
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/814,279
(B) FILING DATE: 10-MAR-1997
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Sarah B. Adriano
(B) REGISTRATION NUMBER: 34,470
(C) REFERENCE/DOCKET NUMBER: 30435.54USI2
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 626-395-7801
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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 998 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...998

(D) OTHER INFORMATION: Human PSCA nucleotide sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGGGAGAGGC	AGTGACCATG	AAGGCTGTGC	TGCTTGCCCT	GTTGATGGCA	GGCTTGGCCC	60
TGCAGCCAGG	CACTGCCCTG	CTGTGCTACT	CCTGCAAAGC	CCAGGTGAGC	AACGAGGACT	120
GCCTGCAGGT	GGAGAACTGC	ACCCAGCTGG	GGGAGCAGTG	CTGGACCGCG	CGCATCCGCG	180
CAGTTGGCCT	CCTGACCGTC	ATCAGCAAAG	GCTGCAGCTT	GAAGTGCCTG	GATGACTCAC	240
AGGACTACTA	CGTGGGCAAG	AAGAACATCA	CGTGCTGTGA	CACCGACTTG	TGCAACGCCA	300
GCGGGGCCCA	TGCCCTGCAG	CCGGCTGCCG	CCATCCTTGC	GCTGCTCCCT	GCACTCGGCC	360
TGCTGCTCTG	GGGACCCGGC	CAGCTATAGG	CTCTGGGGGG	CCCCGCTGCA	GCCCACACTG	420
GGTGTGGTGC	CCCAGGCCCT	TGTGCCACTC	CTCACAGAAC	CTGGCCCAGT	GGGAGCCTGT	480
CCTGGTTCCCT	GAGGCACATC	CTAACGCAAG	TTTGACCATG	TATGTTTGCA	CCCCTTTTCC	540
CCNAACCCTG	ACCTTCCCCT	GGGCCTTTTC	CAGGATTCCN	ACCNGGCAGA	TCAGTTTTAG	600
TGANACANAT	CCGCNTGCAG	ATGGCCCCCT	CAACCNNTTN	TGTTGNTGTT	TCCATGGCCC	660
AGCATTTTCC	ACCCTTAACC	CTGTGTTTCAG	GCACCTTNTTC	CCCCAGGAAG	CCTTCCCCTGC	720
CCACCCCAT	TATGAATTGA	GCCAGGTTTG	GTCCGTGGTG	TCCCCCGCAC	CCAGCAGGGG	780
ACAGGCAATC	AGGAGGGCCC	AGTAAAGGCT	GAGATGAAGT	GGACTGAGTA	GAAGTGGAGG	840
ACAAGAGTTG	ACGTGAGTTC	CTGGGAGTTT	CCAGAGATGG	GGCCTGGAGG	CCTGGAGGAA	900
GGGGCCAGGC	CTCACATTTG	TGGGNTCCC	GAATGGCAGC	CTGAGCACAG	CGTAGGCCCT	960
TAATAAACAC	CTGTTGGATA	AGCCAAAAAA	AAAAAA			998

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...123

(D) OTHER INFORMATION: Human PSCA amino acid sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Lys	Ala	Val	Leu	Leu	Ala	Leu	Leu	Met	Ala	Gly	Leu	Ala	Leu	Gln	
1				5				10					15			
Pro	Gly	Thr	Ala	Leu	Leu	Cys	Tyr	Ser	Cys	Lys	Ala	Gln	Val	Ser	Asn	
			20					25					30			
Glu	Asp	Cys	Leu	Gln	Val	Glu	Asn	Cys	Thr	Gln	Leu	Gly	Glu	Gln	Cys	
		35					40					45				
Trp	Thr	Ala	Arg	Ile	Arg	Ala	Val	Gly	Leu	Leu	Thr	Val	Ile	Ser	Lys	
	50					55					60					
Gly	Cys	Ser	Leu	Asn	Cys	Val	Asp	Asp	Ser	Gln	Asp	Tyr	Tyr	Val	Gly	
65				70					75					80		
Lys	Lys	Asn	Ile	Thr	Cys	Cys	Asp	Thr	Asp	Leu	Cys	Asn	Ala	Ser	Gly	
			85					90						95		
Ala	His	Ala	Leu	Gln	Pro	Ala	Ala	Ala	Ile	Leu	Ala	Leu	Leu	Pro	Ala	
			100					105					110			

Leu Gly Leu Leu Leu Trp Gly Pro Gly Gln Leu
115 120

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...441
- (D) OTHER INFORMATION: mPSCA nucleotide sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGAAGACAG TTTT TTTTAT CCTGCTGGCC ACCTACTTAG CCCTGCATCC AGGTGCTGCT 60
CTGCAGTGCT ATTCATGCAC AGCACAGATG AACACAGAG ACTGTCTGAA TGTACAGAAC 120
TGCAGCCTGG ACCAGCACAG TTGCTTTAÇA TCGCGCATCC GGGCCATTGG ACTCGTGACA 180
GTTATCAGTA AGGGCTGCAG CTCACAGTGT GAGGATGACT CGGAGAACTA CTATTTGGGC 240
AAGAAGAACA TCACGTGCTG CTAÇTCTGAÇ CTGTGCAATG TCAACGGGGC CCACACCCTG 300
AAGCCACCCA CCACCCTGGG GCTGCTGACC GTGCTCTGCA GCCTGTTGCT GTGGGGCTCC 360
AGCCGTCTGT AGGCTCTGGG AGAGCCTACC ATAGCCCGAT TGTGAAGGGA TGAGCTGCAC 420
TCCACCCAC CCCCACACAG G 441

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...123
- (D) OTHER INFORMATION: mPSCA amino acid translation

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Lys Thr Val Phe Phe Ile Leu Leu Ala Thr Tyr Leu Ala Leu His
1 5 10 15
Pro Gly Ala Ala Leu Gln Cys Tyr Ser Cys Thr Ala Gln Met Asn Asn
20 25 30
Arg Asp Cys Leu Asn Val Gln Asn Cys Ser Leu Asp Gln His Ser Cys
35 40 45
Phe Thr Ser Arg Ile Arg Ala Ile Gly Leu Val Thr Val Ile Ser Lys
50 55 60
Gly Cys Ser Ser Gln Cys Glu Asp Asp Ser Glu Asn Tyr Tyr Leu Gly
65 70 75 80
Lys Lys Asn Ile Thr Cys Cys Tyr Ser Asp Leu Cys Asn Val Asn Gly
85 90 95
Ala His Thr Leu Lys Pro Pro Thr Thr Leu Gly Leu Leu Thr Val Leu
100 105 110

Cys Ser Leu Leu Leu Trp Gly Ser Ser Arg Leu
115 120

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Lys Ile Phe Leu Pro Val Leu Leu Ala Ala Leu Leu Gly Val Glu
1 5 10 15
Arg Ala Ser Ser Leu Met Cys Phe Ser Cys Leu Asn Gln Lys Ser Asn
20 25 30
Leu Tyr Cys Leu Lys Pro Thr Ile Cys Ser Asp Gln Asp Asn Tyr Cys
35 40 45
Val Thr Val Ser Ala Ser Ala Gly Ile Gly Asn Leu Val Thr Phe Gly
50 55 60
His Ser Leu Ser Lys Thr Cys Ser Pro Ala Cys Pro Ile Pro Glu Gly
65 70 75 80
Val Asn Val Gly Val Ala Ser Met Gly Ile Ser Cys Cys Gln Ser Phe
85 90 95
Leu Cys Asn Phe Ser Ala Ala Asp Gly Gly Leu Arg Ala Ser Val Thr
100 105 110
Leu Leu Gly Ala Gly Leu Leu Leu Ser Leu Leu Pro Ala Leu Leu Arg
115 120 125
Phe Gly Pro Leu Leu Leu Trp Gly Pro Gly Gln Leu
130 135 140

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln
1 5 10 15
Pro Gly Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala Gln Val Ser Asn
20 25 30
Glu Asp Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys
35 40 45
Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys
50 55 60
Gly Cys Ser Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly
65 70 75 80
Lys Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys Asn Ala Ser Gly
85 90 95
Ala His Ala Leu Gln Pro Ala Ala Ala Ile Leu Ala Leu Leu Pro Ala
100 105 110

Leu Gly Leu Leu Leu Trp Gly Pro Gly Gln Leu
115 120

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Lys Thr Val Leu Phe Leu Leu Leu Ala Thr Tyr Leu Ala Leu His
1 5 10 15
Pro Gly Ala Ala Leu Gln Cys Tyr Ser Cys Thr Ala Gln Met Asn Asn
20 25 30
Arg Asp Cys Leu Asn Val Gln Asn Cys Ser Leu Asp Gln His Ser Cys
35 40 45
Phe Thr Ser Arg Ile Arg Ala Ile Gly Leu Val Thr Val Ile Ser Lys
50 55 60
Gly Cys Ser Ser Gln Cys Glu Asp Asp Ser Glu Asn Tyr Tyr Leu Gly
65 70 75 80
Lys Lys Asn Ile Thr Cys Cys Tyr Ser Asp Leu Cys Asn Val Asn Gly
85 90 95
Ala His Thr Leu Lys Pro Pro Thr Thr Leu Gly Leu Leu Thr Val Leu
100 105 110
Cys Ser Leu Leu Leu Trp Gly Ser Ser Arg Leu
115 120